

Katherine C. Harris Amrine

Postdoctoral Researcher, UC Davis

e-mail: kc.amrine@gmail.com

website: katieamrine.weebly.com • [git: github.com/kcamrine](https://github.com/kcamrine)

Interests

Genomics, Computational Biology, Bioinformatics and Data Science

Education

- Quantitative and Systems Biology (QSB), University of California, Merced Ph.D. 2008 – 2013
Committee: Carolin Frank (chair), Meng-Lin Tsao, Suzanne Sindi, David Ardell (Adviser)
- Molecular Biology, University of Wyoming B.S. 2003 – 2008
Research Adviser: David Liberles
- Mathematics, University of Wyoming B.S. 2003 – 2008
- Simi Valley High School, Simi Valley, California High School Diploma 1999-2003

Research Experience

- Postdoctoral Researcher, UC Davis Department of Viticulture and Enology, Adviser: Dr. Dario Cantu; *Co-expression network and RNAseq analysis of grapevines and grapevine pathogens* 2013-Present
- Graduate Student, UC Merced Quantitative and Systems Biology Group, Adviser: Dr. David Ardell; *Computational work developing a novel method utilizing full genomic sets of transfer RNAs to estimate deep phylogeny of biased bacterial data. Data curation, statistical analysis, and machine learning applied.* 2008 – 2013
- Undergraduate Research intern, Iowa State Bioinformatics and Computational Biology Program, Adviser: Dr. Edward Yu; *Experimental work in Alanine Scanning: production, purification, and analysis of mutant proteins of a multidrug recognition protein to identify active site residues.* 2007
- Undergraduate Researcher, University of Wyoming Molecular Biology Department, Adviser: Dr. David Liberles; *Computational work to identify regions of elevated positive selection in Embryophyte gene sets along select lineages.* 2006-2008

Teaching Experience

- Invited lecture on Introduction to Machine Learning for Bioinformatics May 6, 2013

- Introduction to Scientific Data Analysis Instructor of Record (MATH15) Fall 2012
- Calculus I Teaching Assistant (MATH21) Spring 2012
- Introduction to Data Analysis Teaching Assistant (MATH15) Fall 2011
- Calculus I Teaching Assistant (MATH11, MATH21) Summer 2011, Spring 2012
- Bioinformatics Teaching Assistant (BIO182) Spring 2009, Spring 2013
- Calculus II Teaching Assistant (MATH22) Fall 2008
- High School Biology, Algebra II, Computer Science Workshop instructor Summer 2008

Scholarships and Extended Education

- Completed 6 of 9 *Coursera* courses in the Data Science Specialization. 7th in progress. Fall 2014 - Present
- QSB Summer Fellowship, UC Merced Summer 2013
- Level 3 Instructional Intern, UC Merced Spring 2013
- GRC Summer Fellowship, UC Merced Summer 2012
- GRC Summer Fellowship, UC Merced Summer 2011
- REU: Computational and Systems Biology, Iowa State University; 2 week course completion in Computational and Systems Biology Summer 2007
- Theodor Hanekamp Memorial Scholarship for Undergraduates in Bioinformatics Fall 2006
- Wyoming NSF EPSCoR: Research Fellowship Summer 2006
- Western Undergraduate Exchange Scholarship 2003-2008

Professional Recognition

- UC Merced Legacy Award, University of California, Merced Fall 2013
- University of California, Merced Outstanding Woman Spring 2011
- Leadership Award: Service to Student Affairs, University of California, Merced Fall 2009 – Spring 2010
- Outstanding Graduate Student, University of California, Merced Fall 2008 - Spring 2009

Professional Service

- University of California, Merced Graduate Student Association Secretary Fall 2012 – Summer 2013
- University of California, Merced Graduate Student Association Campus Affairs Officer (acting President) Fall 2009 – Summer 2011
- QSB 1st Annual Graduate Research Retreat Organizer Spring 2009

Notable Committee Service

- School of Natural Sciences Assistant Dean Search Committee, UC Merced; Graduate student representative Fall 2012
- Graduate School Associate Dean Search Committee, UC Merced; Graduate student representative Fall 2011
- Chancellor's Committee on Campus Climate, Culture and Inclusion; Graduate student representative Fall 2010- Spring 2011
- University of California, Merced Chancellor Selection Committee; Graduate student representative Fall 2010 – Spring 2011
- Graduate and Research Council; Graduate student representative Fall 2009 – Spring 2011

Skills

- Wet Lab: Poly-Acrylamide Gel Electrophoresis, Fluorescence Polarization, Protein Purification, PCR, Alanine Scanning
- Computer Lab: Extensive Programming in Perl, R, Darwin, Moderate Programming in Java, C++, Python; Operate in UNIX environment; Machine learning and Statistical Analysis; RNAseq data processing and analysis; Microarray data processing and analysis;

Publications

- Blanco-Ulate, B., Amrine, K.C.H., Collins, T.S., Rivero, R.M., Vicente, A.R., Morales-Cruz, A., Doyle, C.L., Ye, Z., Allen, G., Heymann, H., Ebeler, S.S., Cantu, D. 2015, "Developmental and metabolic plasticity of ripe Sémillon grape berries in response to Botrytis cinerea during noble rot" *Under Review*
- Amrine, K.C.H., Blanco-Ulate, B., Riaz, S., Pap, D., Jones, L., Figueroa-Balderas, R., Walker, A.M., Cantu, D. 2015, "Comparative transcriptomics of Central Asian *Vitis vinifera* accessions with partial resistance to powdery mildew." *Under Review*
- Morales-Cruz, A., Amrine, K.C.H., Blanco-Ulate, B., Lawrence, D.P., Travadon, R., Rolshausen, P., Baumgartner, K., Cantu, D. 2015, "Distinctive expansion of gene families associated with plant cell wall

degradation, secondary metabolism, and nutrient uptake in the genomes of grapevine trunk pathogens.” BMC Genomics. 16:469

- Lawrence, T.J., Kauffman, K.T., Amrine, K.C.H., Carper, D.L, Lee, R.S., Becich, P.J, Canales, C.J, Ardell, D.H. 2015, “FAST: FAST Analysis of Sequences Toolbox.” *Frontiers in Genetics*. 6:172.
- Amrine, K.C.H., Blanco-Ulate, B. Cantu, D. 2014, “Discovery of core biotic stress responsive genes in Arabidopsis by weighted gene co-expression network analysis”. *PLoS One*. 10(3): e0118731.
- Jones, L., Riaz, S., Morales-Cruz, A., Amrine, K.C.H., McGuire, B., Gubler, D.W., Walker, A.M., Cantu, D. 2014, “Adaptive Genomic Structural Variation in the Grape Powdery Mildew Pathogen, *Erysiphe necator*. *BMC Genomics*, 15:1081.
- Blanco-Ulate, B., Morales-Cruz, A., Amrine, K.C., Labavitch, J.M., Powell, A., Cantu, D. 2014, “Genome wide transcriptional profiling of *Botrytis cinerea* genes targeting plant cell walls during infections of different hosts.” *Frontiers in Plant Science*, 5:435.
- Amrine, K.C.H., Swingley W.D., and Ardell D.A. 2014. “tRNA signatures reveal polyphyletic origins of streamlined SAR11 genomes among the Alphaproteobacteria.” *PLoS Computational Biology*, 10(2): e1003454
- Huzurbazar, S., Kolesov, G., Massey, S.E., Harris, K.C., Churbanov, A., and Liberles, D.A. 2010. “Lineage-specific differences in the amino acid substitution process.” *Journal of Molecular Biology*, 396:1410-1421.
- Li, M., Gu, R., Su, C.-C., Routh, M.D., Harris, K.C., Jewell, E.S., McDermott, G., and Yu, E.W. 2007. “Crystal structure of the transcriptional regulator AcrR from *Escherichia coli*.” *Journal of Molecular Biology* 374:591-603.

Posters

- Society for Molecular Biology and Evolution (SMBE) international conference, Chicago, CA “Phylogenetically Informative tRNA Signatures are Robust to Base Convergence and Horizontal Gene Transfer” July ,2014
- 2013 Bay Area RNA Club (BARC), San Francisco, CA “tRNA Class-Informative Features” March 12
- 112th Annual Meeting of the American Society for Microbiology, San Francisco, CA. “Using tRNA Functional Elements to Identify and Phylogenetically Classify *Alphaproteobacteria*.” June 18, 2012
- 15th Annual Meeting of the RNA Society, Seattle, WA. “Information Statistical Analysis to Uncover *trm10* Modification Determinants in tRNAs in Yeast.” June 26, 2010
- Research Week, University of California, Merced. “Information Statistical Analysis to Uncover *trm10* Modification Determinants in tRNAs in Yeast.” April 13, 2010

Talks

- The 5th Western Evolutionary Biology Meeting, Irvine, CA. “Phylogenetically informative tRNA signatures are robust to base convergence and horizontal gene transfer.” May 11, 2013

- The First Joint Congress on Evolutionary Biology, Ottawa, ON. “Detecting and Resolving Inconsistencies in Deep Roots of the Tree of Life.” July 10, 2012
- UC Merced QSB Fall Retreat, Mariposa, California, “Detecting and Resolving Inconsistencies in Deep Roots of the Tree of Life.” October 22, 2011
- The University of Wyoming, Laramie, Wyoming; “Improved Estimation of Logo Bias and Significance with Application to Estimating Phylogeny with tRNA Identity Elements.” March 31, 2011
- Uppsala University, Uppsala, Sweden; “Information Statistical Analysis to Uncover *trm10* Modification Determinants in tRNAs in yeast.” April 28, 2010
- University of Strasbourg, Strasbourg, France; “Information Statistical Analysis to Uncover *trm10* Modification Determinants in tRNAs in yeast.” April 19, 2010
- The Ohio State University, Columbus, Ohio; “Information Statistical Analysis to Uncover *trm10* Modification Determinants in tRNAs in yeast.” March 9, 2010